SEQUENCE LISTING <110> Godfrey, Wayne Buck, David Engleman, Edgar G. <120> Receptor on the Surface of Activated T-Cells: ACT-4 <130> 16524.010 <150> US 08/472,940 <151> 1995-06-06 <150> US 08/147,784 <151> 1993-11-03 <160> 2 <210> 1 <211> 1058 <212> DNA <213> Homo sapiens <220> <221> CDS <223> (15)..(845) <220> <223> ACT-4-h-1 cDNA <400> 1 cagcagagac gagg atg tgc gtg ggg gct cgg cgg ctg ggc cgc ggg ccg Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro tgt gcg gct ctg ctc ctc ctg ggc ctg ggg ctg agc acc gtg acg ggg 98 Cys Ala Ala Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly 20 ctc cac tgt gtc ggg gac acc tac ccc agc aac gac cgg tgc tgc cac 146 Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His 35 gag tgc agg cca ggc aac ggg atg gtg agc cgc tgc agc cgc tcc cag 194 Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln

50

65

aac acg gtg tgc cgt ccg tgc ggg ccg ggc ttc tac aac gac gtg gtc

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val

age tee aag eeg tge aag eec tge aeg tgg tgt aac ete aga agt ggg

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly

agt gag egg aag eag etg tge aeg gee aea eag gae aea gte tge ege

242

290

338

Ser	Glu	Arg 95	Lys	Gln	Leu	Cys	Thr 100	Ala	Thr	Gln	Asp	Thr 105	Val	Cys	Arg	
-					cag Gln		-	_	_		_			_	_	386
-	-		_		cca Pro 130						~ -	_		-	_	434
					aac Asn											482
_	-	_		_	tcg Ser	_	-		_		_		_			530
_	_	-		_	gag Glu		_			-	-					578
					gcc Ala						_					626
					ccc Pro 210						-	-		_		674
					ggg Gly											722
					agg Arg											770
					agt Ser											818
					ctg Leu				tga	cctt	gggc	cca	ccaa	ggt		866
gga	ggacgctggg ccccgccagg ctggagcccg gagggtctgc tgggcgagca gggcaggtgc														aggtgc	926
agg	aggccgcctg eecegccacg cteetgggcc aactetgcac egttetaggt geegatgget														986	
gcc	tccg	gct (ctct	gctta	ac gt	tatg	ccat	g cat	tacc	tcct	gcc	ccgc	ggg a	acca	caataa	1046
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<223> deduced amino acid sequence of ACT-4-h-1

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Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys 50 55 60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro 65 70 75 80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys 85 90 95

Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys 115 120 125

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp 130 135 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn 145 150 155

Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
165 170 175

Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr 180 185 190

Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu 195 200 205

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val 210 215220

Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu 225 230 235 240

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly 245 250 255

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser 260 265 270

Thr Leu Ala Lys Ile 275

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